

SEQUENCE LISTINGS

5 SEQ ID NO. 1

SEQ ID No. 1 is the amino acid sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

10

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HSPDE1B1  MELSPRSPPEMLEESDCPSFLELKSAPSKMWIKLRSLRLRYMVKQLENGEINIEELKKNL
HSPDE1B2  -----MANPVPVQRSHLQGPILRLR-----YMKQLENGEINIEELKKNL
          ..*: :: : : : :*: *****
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15

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HSPDE1B1  EYTASLLEAVYIDETRQILDTDELQELRSDAVPSEVRDWLASTFTQARAKGRRAEEKP
HSPDE1B2  EYTASLLEAVYIDETRQILDTDELQELRSDAVPSEVRDWLASTFTQARAKGRRAEEKP
          *****
```

20

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HSPDE1B1  KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADHAL
HSPDE1B2  KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADHAL
          *****
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25

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HSPDE1B1  RTIVFELLTRNLIISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
HSPDE1B2  RTIVFELLTRNLIISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
          *****
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30

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HSPDE1B1  RTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSFHIQTKSECAIVNDRSVLENHHISSV
HSPDE1B2  RTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSFHIQTKSECAIVNDRSVLENHHISSV
          *****
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35

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HSPDE1B1  FRLMQDDENMIFINLTKEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
HSPDE1B2  FRLMQDDENMIFINLTKEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
          *****
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40

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HSPDE1B1  ALSLLLHAADISHPTKQWLVSRTWKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
HSPDE1B2  ALSLLLHAADISHPTKQWLVSRTWKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
          *****
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45

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HSPDE1B1  QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
HSPDE1B2  QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
          *****
```

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HSPDE1B1  FRSTWVKRIQENKQKWERAASGITNQMSIDELSPCEEEAPPSPAEDHNQNGNLD
HSPDE1B2  FRSTWVKRIQENKQKWERAASGITNQMSIDELSPCEEEAPPSPAEDHNQNGNLD
          *****
```

Sub B13

005760 7012550

SEQ ID NO. 2

5 SEQ ID No. 2 is the nucleotide sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

10 HSPDE1B1 GTGACCCACAGCTCCGCCCAAGCGTCCGGCCTAGAGACACCGGCCTGGCTGGTCCACGC
HSPDE1B2 GTGACCCACAGCGTCCGGG-AGGAGGAAGGC--AGGGGCCAAGAGGAAGTTGTCCCCTC
***** * * * **

15 HSPDE1B1 CAGCCGCAGACCGTGGCTGAGCATGGAGCTGTCCCCCGCAGTCCTCCGGAGATGCTGGA
HSPDE1B2 TTGGGGG---CCCTGGG-GCTCCTGGGG-T-C--AGGATTTTGATACTCTGAAGCAGGA
* * * * *

20 HSPDE1B1 GGAGTCGGATTGCCC--GTCACCCCTGGAGCTGAAGTCAGCCCCCAGAAGAAGATGTGG
HSPDE1B2 A-ACTTTGATTCCCATGGCAAACCCTGTTCTGTTCAGAGGCCACCTCCAGG-----
* * **** * * ***** ** * * *

25 HSPDE1B1 ATTAAGCTTCGCTCTCTG-CTGCCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
HSPDE1B2 ----GCCCCATTCTCAGGCTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
* * * **** * *****

30 HSPDE1B1 CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT
HSPDE1B2 CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT

35 HSPDE1B1 AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTGATGCT
HSPDE1B2 AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTGATGCT

HSPDE1B1 CGTGCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTACCCAGCAGGCCCGGGCCAA
HSPDE1B2 CGTGCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTACCCAGCAGGCCCGGGCCAA

HSPDE1B1 AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCCGAAGCATTGTGCAGCTGTGCAGGCTGG
HSPDE1B2 AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCCGAAGCATTGTGCAGCTGTGCAGGCTGG

40 HSPDE1B1 GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
HSPDE1B2 GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC

45 HSPDE1B1 TGCGGTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTCTCTGAA
HSPDE1B2 TGCGGTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTCTCTGAA

50 HSPDE1B1 CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTGAGTTGCTGACTCGGCATAA
HSPDE1B2 CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTGAGTTGCTGACTCGGCATAA

HSPDE1B1 CCTCATCAGCCGCTTCAAGATCCCACTGTGTTTTGATGAGTTTCTGGATGCCTTGGA
HSPDE1B2 CCTCATCAGCCGCTTCAAGATCCCACTGTGTTTTGATGAGTTTCTGGATGCCTTGGA

55 HSPDE1B1 GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
HSPDE1B2 GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC

60 HSPDE1B1 CCAGACAGTCCATTGCTTCTTGTCTCCGCACAGGATGGTGCAGTGCCTGTCCGAGATTGA
HSPDE1B2 CCAGACAGTCCATTGCTTCTTGTCTCCGCACAGGATGGTGCAGTGCCTGTCCGAGATTGA

65 HSPDE1B1 GCTCCTGGCCATCATCTTGTCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
HSPDE1B2 GCTCCTGGCCATCATCTTGTCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA

70 HSPDE1B1 CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGACAATGATCGTTCAGTGCT
HSPDE1B2 CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGACAATGATCGTTCAGTGCT

HSPDE1B1 GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
HSPDE1B2 GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT

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HSPDE1B1 CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGT
 HSPDE1B2 CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGT

 5
 HSPDE1B1 GGCCACAGACATGTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
 HSPDE1B2 GGCCACAGACATGTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA

 10
 HSPDE1B1 GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGTCTCATGTGCTGACATCAG
 HSPDE1B2 GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGTCTCATGTGCTGACATCAG

 15
 HSPDE1B1 CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT
 HSPDE1B2 CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT

 20
 HSPDE1B1 CTTCCTCAGGGTGACAAGGAGGCAGAGTTGGGCCGTCCTTTTCTCCACTCTGTGACCG
 HSPDE1B2 CTTCCTCAGGGTGACAAGGAGGCAGAGTTGGGCCGTCCTTTTCTCCACTCTGTGACCG

 25
 HSPDE1B1 CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCAC
 HSPDE1B2 CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCAC

 30
 HSPDE1B1 ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCTGGCGGATGAGGACTC
 HSPDE1B2 ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCTGGCGGATGAGGACTC

 35
 HSPDE1B1 CAAGTCTAAAAACAGCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG
 HSPDE1B2 CAAGTCTAAAAACAGCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG

 40
 HSPDE1B1 AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTGAGGAGAA
 HSPDE1B2 AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTGAGGAGAA

 45
 HSPDE1B1 CAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA
 HSPDE1B2 TAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA

 50
 HSPDE1B1 GCTGTCCCCCTGTGAAGAAGAGGCCCCCATCCCCGCGGAAGATGAACACAACAGAA
 HSPDE1B2 GCTGTCCCCCTGTGAAGAAGAGGCCCCCATCCCCGCGGAAGATGAACACAACAGAA

 55
 HSPDE1B1 TGGGAATCTGGATTAGCCCTGGGGCTGGCCAGGTCTTCATTGAGTCCAAAGTGTGTTGAT
 HSPDE1B2 TGGGAATCTGGATTAGCCCTGGGGCTGGCCAGGTCTTCATTGAGTCCAAAGTGTGTTGAT

 60
 HSPDE1B1 GTCATCAGCACCATCCATCAGGACTGGCTCCCCATCTGCTCCAAGGGAGCGTGGTCGTG
 HSPDE1B2 GTCATCAGCACCATCCATCAGGACTGGCTCCCCATCTGCTCCAAGGGAGCGTGGTCGTG

 65
 HSPDE1B1 GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTGGGGTTGGGGAAGGGCCCCCT
 HSPDE1B2 GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTGGGGTTGGGGAAGGGCCCCCT

 70
 HSPDE1B1 CCCCACCTGACACCCACTGGGGTGCACTTTAATGTTCCGGCAGCAAGACTGGGGAACCTC
 HSPDE1B2 CCCCACCTGACACCCACTGGGGTGCACTTTAATGTTCCGGCAGCAAGACTGGGGAACCTC

 75
 HSPDE1B1 AGGCTCCCAGTGGTCACTGTGCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG
 HSPDE1B2 AGGCTCCCAGTGGTCACTGTGCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG

 HSPDE1B1 GCTGCCAGGGAGCGGGAGCTTCTGGAGGCTTCCCAGGGCCTTGGGGAAGGGTCAGAGA
 HSPDE1B2 GCTGCCAGGGAGCGGGAGCTTCTGGAGGCTTCCCAGGGCCTTGGGGAAGGGTCAGAGA

 HSPDE1B1 TGCCAGCCCCCTGGGACCTCCCCATCCTTTTGCCTCCAAGTTTCTAAGCAATACATTT
 HSPDE1B2 TGCCAGCCCCCTGGGACCTCCCCATCCTTTTGCCTCCAAGTTTCTAAGCAATACATTT

 HSPDE1B1 TGGGGTTCCCTCAGCCCCCACCCAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTC
 HSPDE1B2 TGGGGTTCCCTCAGCCCCCACCCAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTTC

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5 HSPDE1B1 CTCCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG
HSPDE1B2 CTCCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG

10 HSPDE1B1 GGGAGGGGAGTGGATTCCCTCAGGGCATGGTACCTTCTAGGACCTGGGAATGGGGTGGG
HSPDE1B2 GGGAGGGGAGTGGATTCCCTCAGGGCATGGTACCTTCTAGGATCTGGGAATGGGGTGGG

15 HSPDE1B1 GAGGACATCCTCTTACACCCAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC
HSPDE1B2 GAGGACATCCTCTTACACCCAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC

20 HSPDE1B1 TGAATCTTCCTTCCTCCCTTTTCTGATATAGTGACTGGGGCAAAGGAGCCATTGTGACC
HSPDE1B2 TGAATCTTCCTTCCTCCCTTTTCTGATACAGTGACTGGGGCAAAGGAGCCATTGTGACC

25 HSPDE1B1 AGGGGCTGCGGGAGGCCTTTCTGGGACCTTCCTTGGGACTGGTCTGGGCCCTGGGGCT
HSPDE1B2 AGGGGCTGCGGGAGGCCTTTCTGGGACCTTCCTTGGGACTGGTCTGGGCCCTGGGGCT

30 HSPDE1B1 TGTCGCCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCTCTCCCCTGGGGCTGGGAGGC
HSPDE1B2 TGTCGCCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCTCTCCCCTGGGGCTGGGAGGC

35 HSPDE1B1 TCCATCCGACCAATGTCTGTAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA
HSPDE1B2 TCCATCCGACCAATGTCTGTAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA

40 HSPDE1B1 TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT
HSPDE1B2 TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT

45 HSPDE1B1 TGCTAAAAGAGAGGGTCTGTCCCCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC
HSPDE1B2 TGCTAAAAGAGAGGGTCTGTCCCCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC

50 HSPDE1B1 ACTAAGAAGCTCCTCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
HSPDE1B2 ACTAAGAAGCTCCTCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG

55 HSPDE1B1 GGGCTCAGGGCTGCTGCCTTCCTGTCTCTGGAGAGAACCAGCCAGGCGCGGTGCCCT
HSPDE1B2 GGGCTCAGGGCTGCTGCCTTCCTGTCTCTGGAGAGAACCAGCCAGGCGCGGTGCCCT

60 HSPDE1B1 TCCTCTCCTCAGGCTCCTCCTTGCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG
HSPDE1B2 TCCTCTCCTCAGGCTCCTCCTTGCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG

65 HSPDE1B1 ACTGCCCTCCTTTCTTTCTGTAATACCAACCGTGCATTGTACAGTGGGCCCTGTTTAT
HSPDE1B2 ACTGCCCTCCTTTCTTTCTGTAATACCAACCGTGCATTGTACAGTGGGCCCTGTTTAT

HSPDE1B1 CCCGAGAAGGGCAGAGACGCATGTGACTACCCCTGCCCTTGGTTTCCCAGACCCCTGCT
HSPDE1B2 CCCGAGAAGGGCAGAGACGCATGTGACTACCCCTGCCCTTGGTTTCCCAGACCCCTGCT

HSPDE1B1 ACAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAA
HSPDE1B2 ATAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAA

SEQ ID No. 1

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-----MANPVPVQRSHLQGPILRLR----YMKQLENGEINIEELKKNL
EYTSALLEAVYIDETQRIIDTEDELQELRSDAVPSEVRDWLASTFTQQRAGKRAAEKPK
KFRSIVHVAQAGIFVERMFRRITYTSVGPTYSTAVLNCLKNLDLWCFDVSFLNQAAADHAL
RTIVFELLTRHNLISREFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTTQTVHCFLL
RTGMVHCLSEITELAIIFAAAHIDYEHTGTTNSFHIQTKSECAIVYNDRSVLHENHISVS
FRLMQDDEMNI FINLTKDEFELRALVIEMVLATDMSCHFQQVTKMTALTQOLERIDKPK
ALSLLLHAADISHPTKQWLHVSRWTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
QIGFIDFIVEPTFSVLTDVAEKSVPQLADESKSNQPSFQWRQPSLDVEVGDPNPDVVS
FRSTWVKRIOENKQWKKERAASGITNQMSIDELSPCEEAPPSPAEDEHNONGNLD

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SEQ ID NO. 2

GTCCAGCCACGCGTCCGGG-AGGAGGAAGGC--AGGGGCCAAAGAGGAAGTTGTCCCTCT
TGGGGG--CCCTGGG-GCTCCTGGGG-T--C--AGGATTTTGATACTCTGAAGCAGGA
A-ACTTTGATTCCCATGGCAAAACCTGTCTCTGTTCAGAGGAGCCACTCCAGG-----
GCCCATCTCTCAGGCTCGCATCTGGTTGAAGCAGTTGGAGAATGGGAGATAAA
CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT
AGATGAGACACGGCAAACTCTTGACACGGGAGGACGAGCTGACGGAGCTCGCGTCAGATGC
CGTGCCTTCGGAGTTCGGGACTGGCTGGCTTCCACTTCCACCGACGAGCCGGCCCA
AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCGGAAGCATTTGTGCACGCTGTGCAGGCTGG
GATCTTCGTGGAACGGATGTTTCGGGAGACATACACCTCTGTGGGCCCCACTTACTCTAC
TGGGTTCTCAACTGCTCAAGAACCTGGATCTCTGTGCTTTTGATGTCTTTTCTTTGAA
CAGGAGCAGCATGACCATGCCCTGAGGACCATGTGTTTTGAGTTGCTGACTCCGGATAA
CCTCATCAGCCGCTTCAAGATTCCCACTGTGTTTTGATGAGTTTCTGGATGCCTTGGA
GACAGGCTATGGGAAGTACAAGATCCTTACCACAACAGCATCCAGCGAGCCGATGTAC
CCAGACAGTCCATTGCTTCTTGCTCCGACAGGAGTGGTGACTGCGCTGTGCGAGATTGA
GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCA
CAGCTTCCACATCCAGACAAGTCAGATGTCGTCATCGTGACATGCTGTTCACTGCT
GGAGAATCACCACTCAGCTCTGTTTCCGATTGATCGAGGATGATGAGATGAACATTT
CATCAACCTCACCAAGATGAGTTTGTAGAATCCGAGCCCTGGTCACTGAGATGGTGTT
GGCCACAGACATGCTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGAACA
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CCACCAACCAAGCAGTGTTGTGTCGACAGCGCTTGGACCAAGGCCCTCATGGGAAGTAT
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CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCAC
ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCCTGGCGGATGAGGACT
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TAAGCAGAAATGGAAGAACGGGCAAGCAAGTGGCATCACCAACAGATGTCATTGACGA
GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCATCCCTGCCGAAGATGAACACAACCAAA
TGGGAATCTGGATTAGCCCTGGGGCTGGCCAGGTCTTCATTGAGTCCAAAGTGTTTGAT
GTCATCAGCACCATCCATCAGAGACTGGCTCCCCATCTGCTCCAAGGAGCGTGGTCTGTG
GAAGAAACAAACCCACTGAAGGCCAAATGCCAGAGATTTGGGTTGGGAAAGGCCCTT
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AGGCTCCAGTGGTCACTGTGCCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG
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TGCCAGCCCCCTGGGAGCTCCCCACTTTTTGGCTCAAGTTTCTAAGCAATACATTT
TGGGGGTTCCCTCAGCCCCCACCACAGATCTTAGCTGGCAGGTCTGGGTGCCCTTTT
CTCCCTCTGGGAAGGGCTGGAATAGGATAGAAGCTGGGGGTTTTAGAGCCCTATGTGTG
GGGAGGGGAGTGGAATTCCTTCGGGATGTTGACTTTCTAGGATCTGGGAATGGGTGGA
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TGAATCTCCTTCCCTCCCTTTCTGATACAGTGAAGTGGGCAAAAGGAGCCATTGTGACC
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GTGCGCTGCCCTGAGTCCGGAGCCCTTGCCTCCTCTCTCCCTGGGCTGGGAGGC
TCCATCCGACCAATGTCTGTAAAGTGCTTTGAGGATCTGGGCAAGCAAGACACTTCAGAA
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TGCTAAAGAAGAGGGTCTGTCCCTCTCTCCAGCTCCAGAAGTGGCCAGCTGCAGGC
ACTAAGAAGCTCCTCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
GGGCTCAGGGCTGCTGCCCTCTGTCTCTGGAGAGAACCCAGCGAGCCGCGGTGCCCT
TCTCTCCTCAGGCTCCTCTTGCCTCCCACTTGCCTCAGGAAGGCAAGCTCAGGTG
ACTGCCCTCCTTCTTCTGTAAATACCAACCATGCATTTGTACAGTGGGCGCTGTTCAT
GCGAAATCCACATCCATGGTCTCTAGACCTGCTACCCTGGTACTTCCACCTACCCAC
CCCGAGAAGGGCAGAGACGCATGTGACTCACCCTGCCCTTGGTTTCCCAGACCTTCTGCT
ATAGCAGAGACAATAAAGAAGTGGAGACCAAGGAAAAAAGGAAAAAAGGAAAAA